SFQ ID NO.1

FIG.1 a

	•
GAATTCCCCCAACAGAGCCAAGCTCTCCATCTAGTGGACAGGGAAGCTAGCAGCAAACC	59(U.PER:SEQ ID NO:1
TTCCCTTCACTACAAAACTTCATTGCTTGGCCAAAAAGAGAGTTAATTCAATGTAGACAT	119 39
CTATGTAGGCAATTAAAAACCTATTGATGTATAAAACAGTTTGCATTCATGGAGGGCAAC	179 59
TAAATACATTCTAGGACTTTATAAAAGATCACTTTTTATTTA	239 79
ATGGATTATCAAGTGTCAAGTCCAATCTATGACATCAATTATTATACATCGGAGCCCTGC	299
M D Y Q V S S P I Y D I N Y Y T S E P C	99
CARARATCAATGTGAAGCAAATCGCAGCCCGCCTCCTGCCTCCGCTCTACTCACTGGTG	359
QKINVKQIAARLLPPLYSLV	119
	419
TTGATCTTTGGGGCAACATGCTGGTCATCCTCATCCTGATAAACTGCAAAAGG	
FIFGFVGNMLVILILINCKR	139
CTEAAGAGCATGACTGACATCTACCTGCTCAACCTGGCCATCTCTGACCTGTTTTTCCTT	479
K S M T D I Y L L N L A I S D L F F L	159
CTTACTGTCCCCTTCTGGGCTCACTATGCTGCCGCCCAGTGGGACTTTGGAAATACAATG	539
T V P F W A H Y A A A Q W D F G N T M	179
TGTCAACTCTTGACAGGGCTCTATTTTATAGGCTTCTTCTCTGGAATCTTCTTCATCATC	599
Q L L T G L Y F I G F F S G I F F I I	199
The state of the s	
CTCCTGACAATCGATAGGTACCTGGCTGTCGTCCATGCTGTTTTGCTTTAAAAGCCAGG	
LLTIDRYLAVVHAVFALKAR	219
ACGGTCACCTTTGGGGTGACAAGTGTGATCACTTGGGTGGTGGCTGTTTTGCGTCT	719
T V T F G V V T S V I T W V V A V F A S	239
CTCCCAGGAATCATCTTTACCAGATCTCAAAAAGAAGGTCTTCATTACACCTGCAGCTCT	779
	259
L P G I I F T R S Q K E G L H Y T C S S	233
CATTTTCCATACA	

CATTTTCCATACA H F P Y

GAATTCCCCCAACAGAGCCAAGCTCTCCATCTAGTGGACAGGGAAGCTAGCAGCAAACC	59 (WPER:SER I) NO:2, 19 (ISWER:SER I) NO.5,
TTCCCTTCACTACAAAACTTCATTGCTTGGCCAAAAAGAGAGTTAATTCAATGTAGACAT	119 39
CTATGTAGGCAATTAAAAACCTATTGATGTATAAAACAGTTTGCATTCATGGAGGGCAAC	179 59
TAAATACATTCTAGGACTTTATAAAAGATCACTTTTTATTTA	239 79
ATGGATTATCAAGTGTCAAGTCCAATCTATGACATCAATTATTATACATCGGAGCCCTGC	299
M D Y Q V S S P I Y D I N Y Y T S E P C	99
CAAAAAATCAATGTGAAGCAAATCGCAGCCCGCCTCCTGCCTCCGCTCTACTCACTGGTG	359
G K I N V K Q I A A R L L P P L Y S L V	119
5. S	
TTCATCTTTGGTTTTGTGGGCAACATGCTGGTCATCCTCATCCTGATAAACTGCAAAAGG	419
FIFGFVGNMLVILINCKR	139
CIGAAGAGCATGACTGACATCTACCTGCTCAACCTGGCCATCTCTGACCTGTTTTTCCTT	479
L K S M T D I Y L L N L A I S D L F F L	159
CTACTGTCCCCTTCTGGGCTCACTATGCTGCCGCCCAGTGGGACTTTGGAAATACAATG	539
T V P F W A H Y A A A Q W D F G N T M	179
TETCAACTCTTGACAGGGCTCTATTTTATAGGCTTCTTCTCTGGAATCTTCTTCATCATC	599
Q O L L T G L Y F I G F F S G I F F I I	199
CTCCTGACAATCGATAGGTACCTGGCTGTCGTCCATGCTGTTTTGCTTTAAAAGCCAGG	659
LLTIDRYLAVVHAVFALKAR	219
ACGGTCACCTTTGGGGTGGCACAAGTGTGATCACTTGGGTGGTGGCTGTGTTTGCGTCT	719
T V T F G V V T S V I T W V V A V F A S	239
CTCCCAGGAATCATCTTTACCAGATCTCAAAAAGAAGGTCTTCATTACACCTGCAGCTCT	779
L P G I I F T R S Q K E G L H Y T C S S	259
CATTTTCCATACAGTCAGTATCAATTCTGGAAGAATTTCCAGACATTAAAGATAGTCATC	839
HFPYSQYQFWKNFQTLKIVI	279

SEQ ID NO.2 FIG.1b

TIG	GGG G	CTG L	GTC V	CTG L	CCG P	CTG	CTT	GTC V	ATG M	GTC V	ATC	TGC	TAC Y	TCG S	GGA G	ATC I	CTA L	AAA K	ACT T	899 299
-	•	_	TGT		- AAT	- GAG				CAC										959
L	L	R	С	R	N	E	K	K	R	H	R	A	V	R	Ļ	I	F	T	Ι	319
ATG. M	ATT I	GTT V	TAT Y	TTT F	CTC L	TTC F	TGG W	GCI A	'CCC	TAC Y	'AAC N	ATT I	GTC V	CTT L	CTC	CTG L	AAC N	ACC T	TTC	1019 339
CAG O	GAA E	TTC	TTT F	GGC G	CTG L	AAT N	AAT N	TGC C	AGT S	AGC S	TCT S	AAC N	AGG R	TTG L	GAC D	CAA Q	GCT A	ATG M	CAG Q	1079 359
GTG.	ACA T	gag e	ACT T	CTT L	GGG G	ATG M	ACG T	CAC H		TGC C	ATC I	AAC N	CCC P	ATC I	ATC I	TAT Y	GCC A	TTT F	GTC V	1139 379
V GGG	-	_	-		_				_						_			-	TTC	1199
G	Ξ	K	F	R	N	Y	L	L	V	F	F	Q	K	H	I	A	K	R	F	399
TGC C			TGT C	TCT S	ATT I	TTC F	CAG Q	CAA Q	GAC E	GCT A	CCC P	GAG E	CGA R	GCA A		TCA S	GTT V	TAC Y	ACC T	1259 419
R	ŪS	ACT T		GAG E	CAG Q	GAA E	ATA I	TCT S	GTG V	GGC G	TTG L	TGA *	CAC	GGA	.CTC	AAG	TGG	GCT	GGT	1319 439
GAC	Ū CCA Ū	GTC	AGA	GTT	GTG	CAC	ATG	GCI	TAG	TTT	TCA	TAC	ACA	GCC	TGG	GCT	GGG	GGT	NGG	1379 459
	u Gnn T	GAG	GTC	TTT	TIT	AAA	AGG	AAG	TTA	CTG	TTA	TAG	AGG	GTC	TAA	GAT	TCA	TCC	ATT	1439 479
11	TIG	GĆA	TCT	GTT	TAA	AGT	AGA	TTA	GAT	CCG	AAT	TC								

SEQ ID NO.2 (SUITE)

FIG.1c

GAATTCCCCCAACAGAGCCAAGCTCTCCATCTAGTGGACAGGGAAGCTAGCAGCAAACC	59(UPPER: SER II) NAS 19(LOWER: SER II) NA. G
TTCCCTTCACTACAAACTTCATTGCTTGGCCAAAAAGAGAGTTAATTCAATGTAGACAT	119 39
CTATGTAGGCAATTAAAAACCTATTGATGTATAAAACAGTTTGCATTCATGGAGGGCAAC	179 59
TAAATACATTCTAGGACTTTATAAAAGATCACTTTTTATTTA	239 79
ATGGATTATCAAGTGTCAAGTCCAATCTATGACATCAATTATTATACATCGGAGCCCTGC M D Y Q V S S P I Y D I N Y Y T S E P C	299 99
CAAAAAATCAATGTGAAGCAAATCGCAGCCCGCCTCCTGCCTCCGCTCTACTCACTGGTG K I N V K Q I A A R L L P P L Y S L V	359 119
TTCATCTTTGGTTTTGTGGGCAACATGCTGGTCATCCTCATCCTGATAAACTGCAAAAGG F I F G F V G N M L V I L I L I N C K R	419 139
CTGAAGAGCATGACTGACCTGCTCAACCTGGCCATCTCTGACCTGTTTTTCCTT K S M T D I Y L L N L A I S D L F F L	479 159
CTTACTGTCCCCTTCTGGGCTCACTATGCTGCCGCCCAGTGGGACTTTGGAAATACAATG T V P F W A H Y A A A Q W D F G N T M	539 179
TGTCAACTCTTGACAGGGCTCTATTTTATAGGCTTCTTCTCTGGAATCTTCTTCATCATC Q L L T G L Y F I G F F S G· I F F I I	599 199
CTCCTGACAATCGATAGGTACCTGGCTGTCGTCCATGCTGTGTTTGCTTTAAAAGCCAGG L L T I D R Y L A V V H A V F A L K A R	659 219
ACGGTCACCTTTGGGGTGACAAGTGTGATCACTTGGGTGGTGGCTGTTTTGCGTCT T V T F G V V T S V I T W V V A V F A S	719 239
CTCCCAGGAATCATCTTTACCAGATCTCAAAAAGAAGGTCTTCATTACACCTGCAGCTCT L P G I I F T R S Q K E G L H Y T C S S	779 259
CATTITCCATACATTAAAGATAGTCATCTTGGGGCTGGTCCTGCCGCTGCTTGTCATGGT H F P Y I K D S H L G A G P A A A C H G	839 279

SEQ ID NO.3

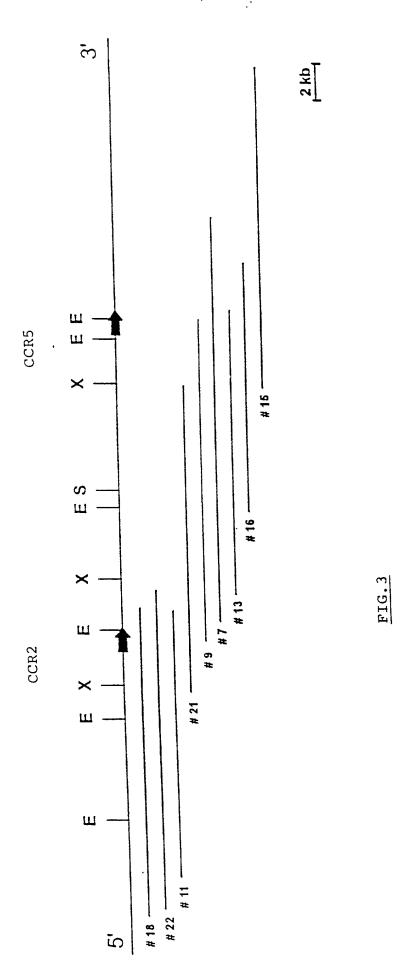
FIG.1d

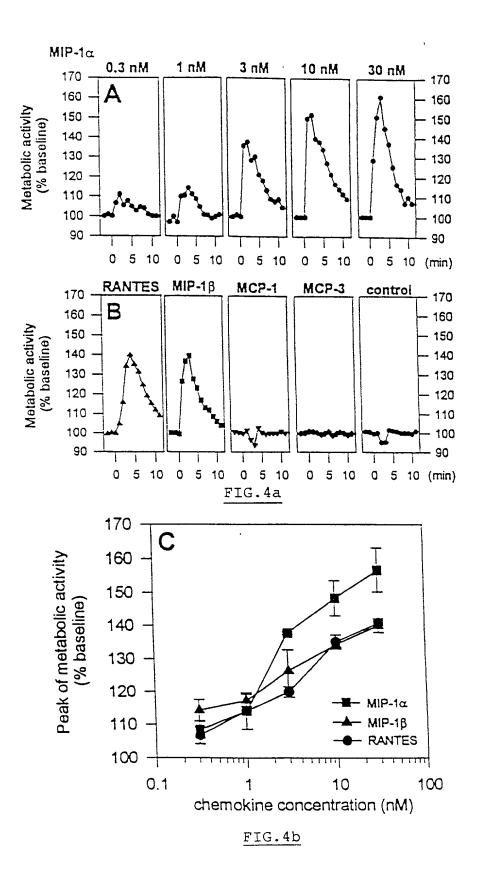
CATCTGCTACTCGGGAATCCTAAAAACTCTGCTTCGGTGTCGAAATGAGAAGAAGAGGCA H L L L G N P K N S A S V S K *	899 299
CAGGGCTGTGAGGCTTATCTTCACCATCATGATTGTTTATTTTCTCTTCTGGGCTCCCTA	959 319
CAACATTGTCCTTCTCCTGAACACCTTCCAGGAATTCTTTGGCCTGAATAATTGCAGTAG	1019 339
CTCTAACAGGTTGGACCAAGCTATGCAGGTGACAGAGACTCTTGGGATGACGCACTGCTG	1079 359
CATCAACCCCATCATCTATGCCTTTGTCGGGGAGAAGTTCAGAAACTACCTCTTAGTCTT	1139 379
CTTCCAAAAGCACATTGCCAAACGCTTCTGCAAATGCTGTTCTATTTTCCAGCAAGAGGC	1199 399
TCCCGAGCGAGCAAGCTCAGTTTACACCCGATCCACTGGGGAGCAGGAAATATCTGTGGG	1259 419
CTTGTGACACGGACTCAAGTGGGCTGGTGACCCAGTCAGAGTTGTGCACATGGCTTAGTT	1319 439
TTEATACACAGCCTGGGGTNGGTTGGNNGAGGTCTTTTTTAAAAGGAAGTTACT	1379 459
GTTATAGAGGGTCTAAGATTCATCCATTTATTTGGCATCTGTTTAAAGTAGATTAGATCC	1439 479
GANITC	

SEQ ID NO.3 (SUITE)
FIG.1e

FIG. 2

	0/14	. 1184	
833 957 87	177 189 182 182 186	272 280 27 276 276	
1 MIYQVSSPIPDINYYTSEPCQMINVKQINANLIEPLYSLVEIFGFVGNMINTLIINCKRIKSMTDIYLLINIAISDINFITTITA 1 MIYQVSSPIPDINYTSEPCQMINVKQINANLIEPLYSLVEIFGFVGNMINVLILINCKRIKSMTDIYLLINIAISDINFITTITA 2 MITTEL MITTEL MATTEL MATT	VEFWALIYA. AAQWDEGNIMOQLITGLYHIGYESGIFFIILLTIDRYLAMVHAVFALKARTVTEGVVTSVITWVVAVFASLEGIIFTRGOKEGIH 1. PLWALESA, ANEWWEGNAMOKHEFGLYHIGYESGIFFIILLTIDRYLAM WHAVFALKARTVTFGVVTSVITWHVAVFASUPGIIFTRGOKEGIH 1. PEWHITYNGHNWYEGHAMOKHISGENITGLYSELFFIILLTIDRYLAM WHAVFAIRARTVTFGVHTSHIMALAIIAANAGHSKTDWEFTH 1. PEWHITYNIKDIWWEGHGHOKHISGENYTGLYSELFFIILLTIDRYLAM WHAVFAIRARTVTFGVHTSHIMALAIIAANAGHSKTDWEFTH 1. PEWITYNIKDIWWEGHGHOKMISWYLVGENSGIEFWHMSIDRYLAM WHAVFAIRHINGWARTVTFGVHTSHIMALAIIAANSTAR	2b riv salar sovoemkne 3 mi sala entenesiaemkie 1 prosi hebbesiremkie R4 mycktry sinst mente	SSHAR DOAMOVTETLGMTHICCINPITYAFVGEKFRATLLVFEGKHTAKR. FCR CSTFGLEAFERASSVYTHSTGEQENSM31. 352 R2D FSFSQ DOARDVTETLGMTHCCINPITYAFVGEKFRATISVFERKHTAKR. FCR CPVEYREPVDGVTFTMHFSTGEQENSM31. 360 R3 ERBKH DIVMINTEVIAYSHCCFANIVIYAFVGERFRATISVEHRINGTANI. LGRYTPFLLYKKHTENISSV. SISTRAFIELISMGF 355 R1 ECSAHLD AMOVTEVIAYFHCCINNIVIYAFVGERFRATIROTEHRRAMI. LMMMLPFLSVDRIERMSST. SISTGENEHSMGF 355 R2 TFERY LDKAHQAFETTAFVHCGINPITYFFIGERFRATIROTEKKMATIROTEKNIGOYGSLLQIYSADTHSSSYTGSTMDHDLHDALI 360
CCR5 hcc-R2b hcc-R3 hcc-R1 hcc-R1	CCR5 hCC-K2b hCC-K3 hCC-K1 hCC-R1	CCR5 hcc-R2b hcc-R3 hcc-R1 hcc-R4	CCR5 hCC-R2b hCC-R3 hCC-R3 hCC-R1





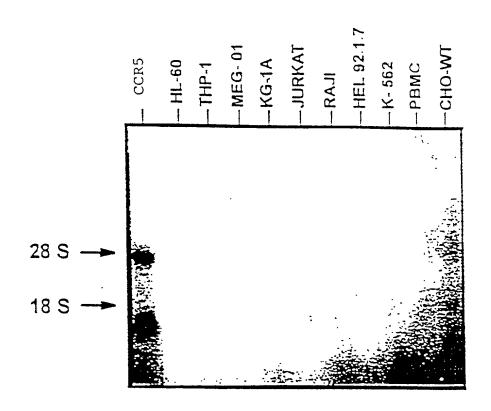
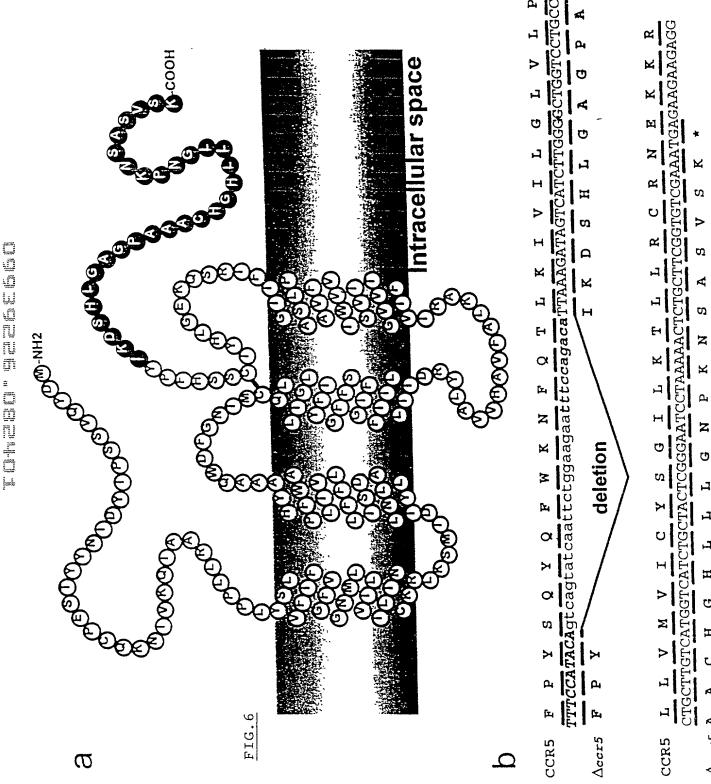
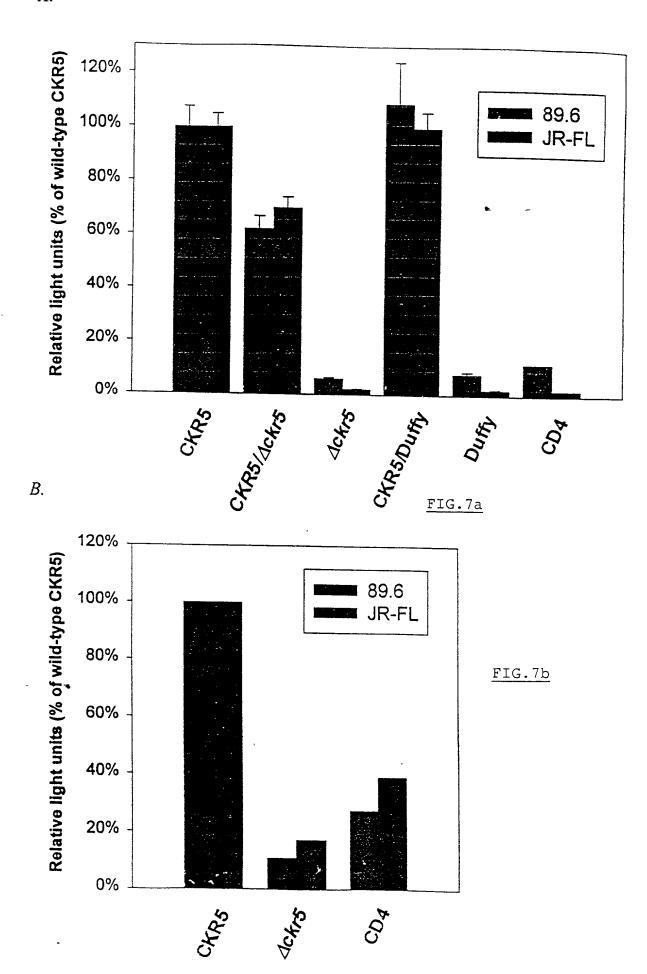


FIG.5





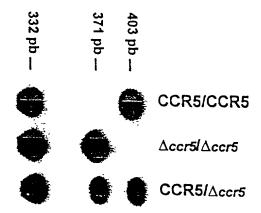


FIG.8

